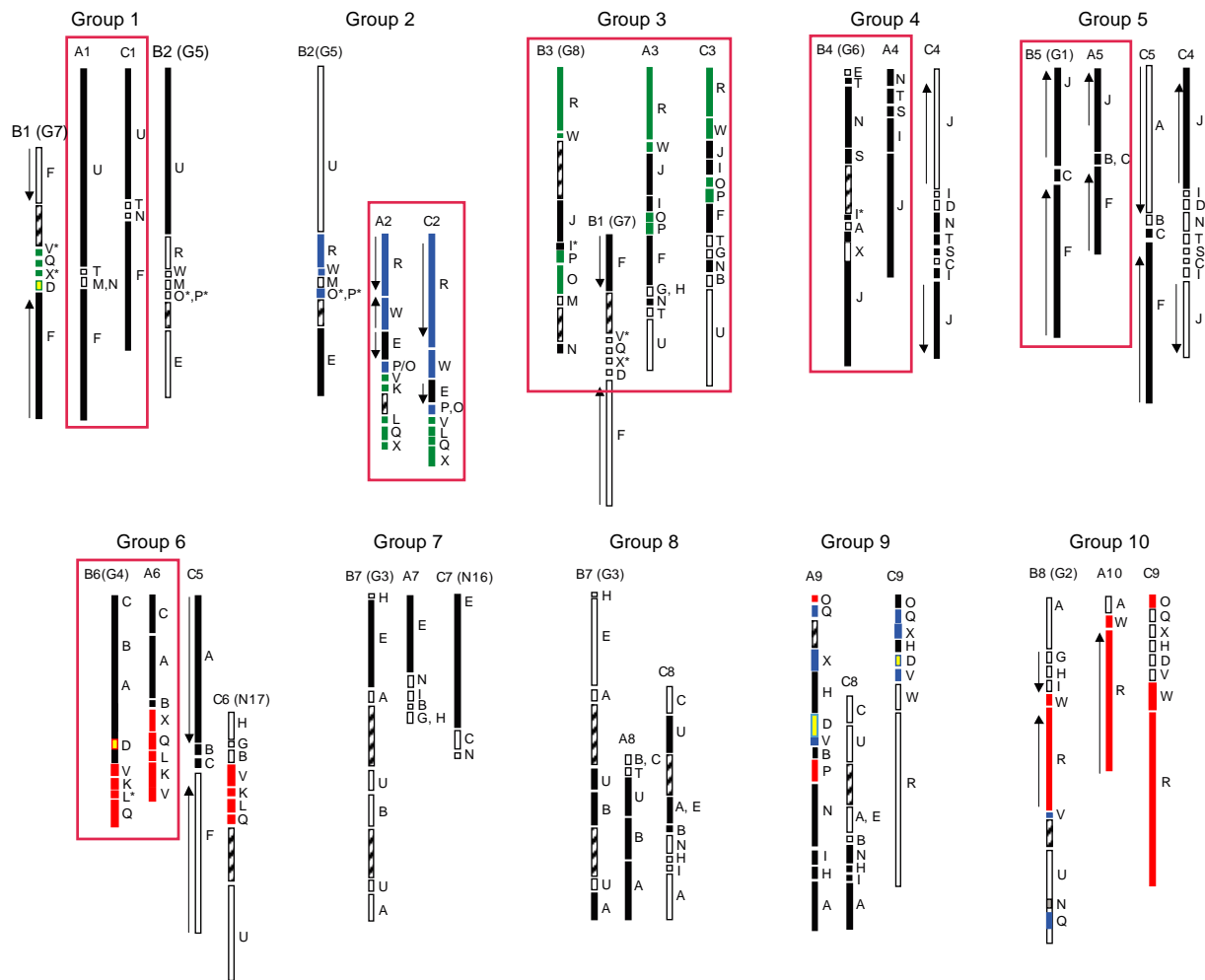


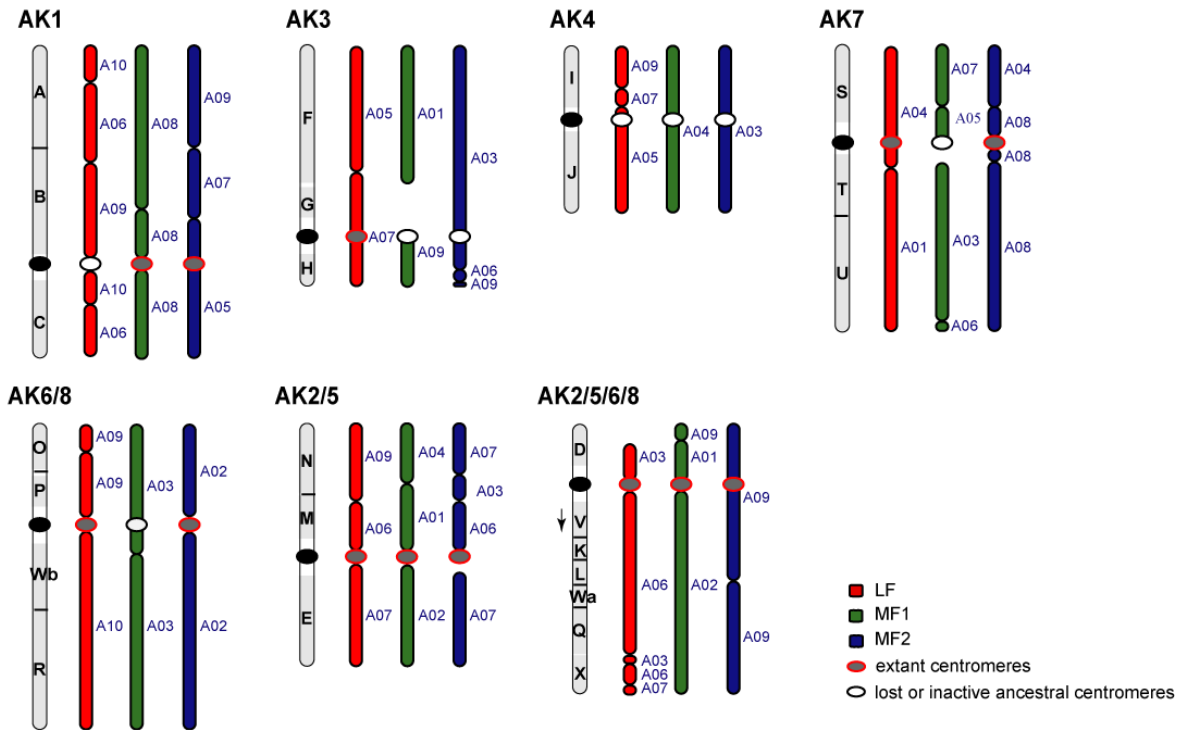
**Supplemental Figure 1. Purported translocation events reshuffling tPCK-specific associations D/V and M/E in the *B. rapa* genome.**

**(A)** Translocation between block  $U_{MF1}$  and block association D/ $V_{LF}$  resulted in block associations Ua/D and V/Ub on *B. rapa* chromosomes A03 and A06, respectively. **(B)** Translocation between two M/E associations from subgenomes LF and MF2 resulted in associations  $M_{LF}/M_{MF2}$  and  $E_{LF}/E_{MF2}$  on chromosomes A06 and A07, respectively.



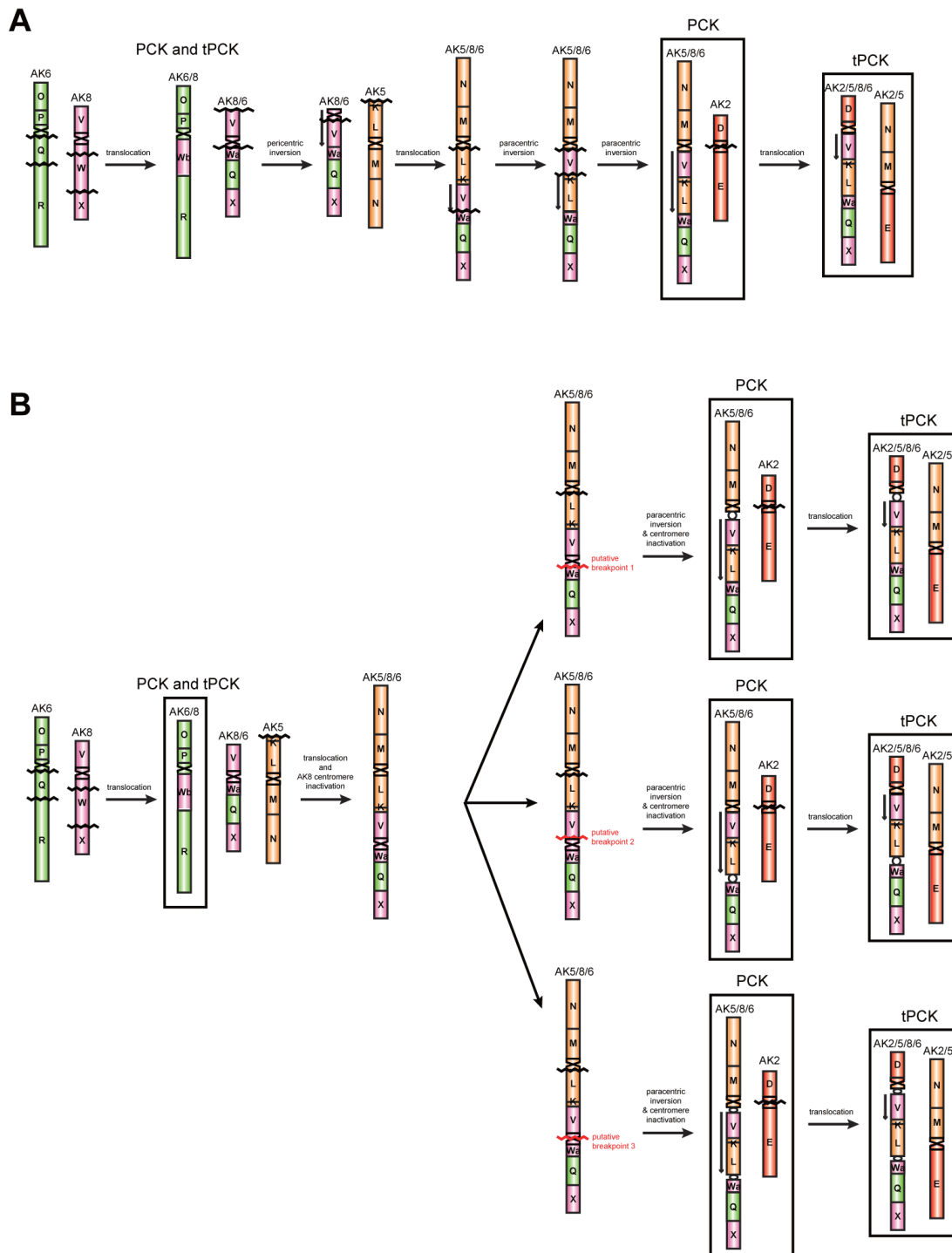
**Supplemental Figure 2. Chromosome collinearity comparison among A, B, and C genomes, revised from Panjabi et al. (2008).**

PCK-specific GB associations O/P/W/R and V/K/L/Q/X are colored to distinguish subgenomes: red = LF, green = MF1, blue = MF2. Within the colored GB associations, each copy of block D associated with block V is indicated in yellow. The entire chromosomes A1 and C1, and A2 and C2 have a similar block orders between A and C genomes; the structures of A4 and B4, A5 and B5, and A6 and B6 are shared between genomes A and B; A3, B3, and C3 share similar chromosome structures between A, B, and C genomes.



**Supplemental Figure 3. Reconstruction of three tPCK-like ancestral subgenomes in *B. rapa*.**

tPCK-like genomes each comprising 24 genomic blocks (A–X) were reconstructed for the three *B. rapa* subgenomes (least fractionated [LF], medium fractionated [MF1], and most fractionated [MF2]). The downward pointing arrow refers to the genomic block inverted relative to the position within the ACK.



**Supplemental Figure 4. Two alternative origins of translocation chromosomes AK5/6/8 (PCK) and AK2/5/6/8 (tPCK).**

Genomic blocks are indicated by capital letters and colored according to their positions on ancestral chromosomes (see Figure 2A). Downward pointing arrows indicate the opposite orientation of GBs compared to their ancestral position within the ACK. Scenario (A) involves a double inversion of genomic block V, whereas alternative (B) is based on a paracentric inversion of V/K/L and accompanying inactivation of the AK8 paleocentromere. The position(s) of the inactivated centromere depend(s) on the position of the inversion breakpoint within the AK8 (peri)centromere.

**Supplemental Table 1.** Summary of genomic blocks identified in *B. rapa*. Red color labels indicate GBs without rearrangements; yellow color labels indicate GBs that were broken; blue color labels indicate GBs with fragmental deletions.

GB	<i>A. thaliana</i>	<i>B. rapa</i> interval		
	interval	LF	MF1	MF2
A	AT1G01560_AT1G02190	Bra033253_Bra033213_A10	Bra030497_Bra030497_A08	Bra032640_Bra032670_A09
	AT1G02220_AT1G07630	Bra033301_Bra015596_A10	Bra030498_Bra030695_A08	Bra032614_Bra031587_A09
	AT1G07640_AT1G19330	Bra018693_Bra025729_A06	Bra030696_Bra016509_A08	Bra031588_Bra031076_A09
B	AT1G19850_AT1G21910	Bra025775_Bra017957_A06	Bra016492_Bra016401_A08	Bra012190_Bra012297_A07
	AT1G21920_AT1G24210	Bra031352_Bra024644_A09	Bra016400_Bra016318_A08	Bra012298_Bra012416_A07
	AT1G24220_AT1G27220	Bra032811_Bra024646_A09	Bra010955_Bra016317_A08	Bra030032_Bra012417_A07
	AT1G27240_AT1G29020	Bra032813_Bra032925_A09	Bra010954_Bra010851_A08	Bra030033_Bra030121_A07
	AT1G29030_AT1G30970	Bra032290_Bra023153_A09	Bra010850_Bra010764_A08	Bra030122_Bra014897_A07
	AT1G30972_AT1G31750	Bra023154_Bra023199_A09	Bra038403_Bra038434_A08	Bra014898_Bra014913_A07
	AT1G31760_AT1G36240	Bra023200_Bra028085_A09	Bra038435_Bra036766_A08	Bra033887_Bra034400_A05
C	AT1G43600_AT1G47260	Bra036926_Bra040713_Scaffold000123	Bra014019_Bra014069_A08	Bra032192_Bra032220_A05
	AT1G47270_AT1G47946	Bra015624_Bra015599_A10	Bra014070_Bra014098_A08	Bra032233_Bra032228_A05
	AT1G47960_AT1G56120	Bra018695_Bra038035_A06	Bra014099_Bra030816_A08	Bra032221_Bra037091_A05
D	AT1G56530_AT1G62045	Bra017901_Bra017885_A03	Bra035468_Bra028377_A01	Bra027924_Bra027067_A09
	AT1G62060_AT1G63770	Bra034461_Bra004106_scaffold	Bra036663_Bra027789_A09	Bra027066_Bra027663_A09
E	AT1G65040_AT1G67210	Bra004109_Bra004209_A07	Bra022497_Bra034014_A02	-
	AT1G67220_AT1G79720	Bra004210_Bra035139_A07	Bra034013_Bra008428_A02	Bra004099_Bra003596_A07
	AT1G79760_AT1G80420	Bra035206_Bra035184_A07	Bra008503_Bra008474_A02	Bra003527_Bra003565_A07
F	AT3G01040_AT3G02070	Bra039149_Bra039109_A05	Bra021479_Bra040520_A01	Bra001025_Bra000980_A03
	AT3G02080_AT3G23150	Bra039150_Bra033888_A05	Bra021478_Bra023756_A01	Bra001028_Bra001904_A03
	AT3G23160_AT3G25520	Bra014914_Bra015128_A07	Bra023755_Bra028373_A01	Bra001905_Bra013215_A03
G	AT2G05170_AT2G10931	Bra015164_Bra015187_A07	-	Bra013178_Bra013160_A03
H	AT2G10940_AT2G17090	Bra015198_Bra002020_A07	Bra037196_Bra037283_A09	Bra013156_Bra013035_A03
	AT2G17110_AT2G19470	Bra002021_Bra039003_A07	Bra037281_Bra036721_A09	Bra009665_Bra024449_A06
	AT2G19480_AT2G20900	Bra039004_Bra036507_A07	Bra036720_Bra036670_A09	Bra031083_Bra031147_A09
I	AT2G20920_AT2G26660	Bra031151_Bra007748_A09	Bra030326_Bra034308_A04	Bra000588_Bra000539_A03
	AT2G26670_AT2G29090	Bra012054_Bra028390_A07	Bra034312_Bra039963_A04	Bra000561_Bra000478_A03
J	AT2G31040_AT2G40420	Bra018282_Bra004963_A05	Bra021690_Bra017005_A04	Bra022823_Bra000184_A03
	AT2G40430_AT2G46130	Bra004567_Bra004962_A05	Bra017004_Bra039289_A04	Bra000185_Bra000413_A03
	AT2G46140_AT2G47730	Bra004566_Bra004434_A05	Bra039288_Bra021440_A04	Bra000414_Bra000460_A03
K	AT2G01250_AT2G03750	Bra024895_Bra025130_A06	Bra014334_Bra026541_A02	Bra017461_Bra017375_A09
L	AT3G25855_AT3G29770	Bra025166_Bra025404_A06	Bra036363_Bra033110_A02	Bra017345_Bra036205_A09
M	AT3G43740_AT3G49970	Bra019444_Bra017958_A06	Bra037606_Bra029985_A01	Bra019453_Bra019606_A06
N	AT3G50950_AT3G51860	Bra036844_Bra006881_A09	Bra038875_Bra038910_A01	Bra012876_Bra012833_A03
	AT3G51870_AT3G52760	Bra006882_Bra006945_A09	Bra033476_Bra019650_A04	Bra012832_Bra012799_A03
	AT3G52770_AT3G62790	Bra006946_Bra007701_A09	Bra019649_Bra014392_A04	Bra028531_Bra003510_A07

<b>O</b>	AT4G00030_AT4G00780	Bra037309_Bra037358_A09	Bra000979_Bra000955_A03	Bra008511_Bra008532_A02
	AT4G00800_AT4G01380	Bra037410_Bra037362_A09	Bra000929_Bra000954_A03	Bra008544_Bra008533_A02
	AT4G01390_AT4G03728	Bra037411_Bra034225_A09	Bra000928_Bra000815_A03	Bra008545_Bra018514_A02
	AT4G03740_AT4G04955	Bra029471_Bra029537_A09	Bra000780_Bra000810_A03	Bra018492_Bra018508_A02
<b>P</b>	AT4G08690_AT4G12070	Bra037874_Bra029437_A09	Bra000655_Bra000760_A03	Bra033210_Bra033122_A02
<b>Q</b>	AT5G23030_AT5G23270	Bra013010_Bra013029_A03	Bra029357_Bra029365_A02	Bra026507_Bra026507_A09
	AT5G23280_AT5G28470	Bra009667_Bra009996_A06	Bra029366_Bra020609_A02	Bra026506_Bra036119_A09
	AT5G28490_AT5G28885	Bra009997_Bra010012_A06	Bra020610_Bra020621_A02	Bra036134_Bra036126_A09
<b>R</b>	AT5G01240_AT5G02000	Bra009636_Bra009646_A10	Bra005693_Bra005657_A03	Bra028894_Bra028918_A02
	AT5G02010_AT5G23010	Bra009621_Bra002448_A10	Bra005701_Bra006645_A03	Bra028883_Bra020228_A02
<b>S</b>	AT5G33210_AT5G37810	Bra028101_Bra028151_A04	Bra039484_Bra039503_A05	Bra038948_Bra035522_A08
	AT5G37830_AT5G41900	Bra028154_Bra025457_A04	Bra028392_Bra028514_A07	Bra025434_Bra030327_A04
<b>T</b>	AT4G12750_AT4G13985	Bra032672_Bra033456_A04	-	Bra034911_Bra040347_A08
	AT4G13990_AT4G14140	Bra032753_Bra032760_A04	-	Bra038960_Bra038444_A08
	AT4G14145_AT4G14490	Bra032763_Bra033481_A04	-	Bra010747_Bra010762_A08
	AT4G14500_AT4G15160	Bra036864_Bra039563_A01	-	Bra039861_Bra038089_A08
	AT4G15180_AT4G16160	Bra039562_Bra033542_A01	Bra012769_Bra012736_A03	Bra038088_Bra038039_A08
	AT4G16162_AT4G16143	Bra033544_Bra033534_A01	Bra012735_Bra012741_A03	Bra021082_Bra038043_A08
<b>U</b>	AT4G16250_AT4G24180	Bra033549_Bra013773_A01	Bra012725_Bra019243_A03	Bra021080_Bra010549_A08
	AT4G24190_AT4G28405	Bra013774_Bra026259_A01	Bra019235_Bra024205_A03	Bra010500_Bra010369_A08
	AT4G28410_AT4G35320	Bra040157_Bra011606_A01	Bra024204_Bra017708_A03	Bra010368_Bra020811_A08
	AT4G35335_AT4G36120	Bra011607_Bra011663_A01	Bra017709_Bra017748_A03	Bra010537_Bra010501_A08
	AT4G36130_AT4G38170	Bra011664_Bra011805_A01	Bra017749_Bra017884_A03	Bra010550_Bra010636_A08
	AT4G38190_AT4G38770	Bra011900_Bra011893_A01	Bra033554_Bra033575_A06	Bra010746_Bra010727_A08
<b>V</b>	AT5G42130_AT5G47780	Bra033636_Bra024917_A06	Bra021948_Bra022156_A02	Bra027974_Bra017467_A09
<b>W</b>	AT5G47820_AT5G50750	Bra037951_Bra037925_A10	Bra000592_Bra000630_A03	Bra020729_Bra022524_A02
	AT5G50760_AT5G60800	Bra035710_Bra002450_A10	Bra022763_Bra006647_A03	Bra022525_Bra020229_A02
<b>X</b>	AT5G60810_AT5G61760	Bra013006_Bra012923_A03	Bra029354_Bra029318_A02	Bra035957_Bra035915_A09
	AT5G61770_AT5G65925	Bra019611_Bra024431_A06	Bra029309_Bra031843_A02	Bra035914_Bra037833_A09
	AT5G65930_AT5G67385	Bra012055_Bra012158_A07	Bra031800_Bra031830_A02	Bra037195_Bra037116_A09

**Supplemental Table 2.** Genomic blocks E, G, and T showing sequence deletion in *B. rapa* (Br) as compared with *Arabidopsis thaliana* (At).

	At block interval	Deleted fragment in Br (subgenome)	Size of deleted fragment % (Mb)
<b>E</b>	AT1G65040 - AT1G80420	AT1G65040 - AT1G67210 (MF2)	3.92% (0.98)
<b>G</b>	AT2G05170 - AT2G17090	AT2G05170 - AT2G17090 (MF1)	100% (5.57)
<b>T</b>	AT4G12750 - AT4G16143	AT4G12750 - AT4G15160 (MF1)	29.82% (1.15)

**Supplemental Table 3.** Number of genomic blocks with different fragmental status in *B. rapa* subgenomes.

	LF	MF1	MF2	Total
<b>Complete</b>	15	16	17	48
<b>Broken</b>	9	6	6	21
<b>Terminal deletion</b>	0	1	1	2
<b>Complete deletion</b>	0	1	0	1
<b>Sum</b>	24	24	24	72

**Supplemental Table 4.** Frequency of tPCK-specific block associations in each of the three *B. rapa* subgenomes.

Chr <sup>a</sup>	GB assoc. <sup>b</sup>	# <sup>c</sup>	LF	MF1	MF2
<b>AK1</b>	A-B	2	A06	A08	-
	B-C	2	-	A08	A05
<b>AK3</b>	F-G	2	A07	-	A03
	G-H	2	A07	-	A03
<b>AK4</b>	I-J	2	-	A04	A03
<b>AK7</b>	S-T	2	A04	-	A08
	T-U	3	A01	A03	A08
<b>AK6/8</b>	O-P	3	A09	A03	A02
	P-W	1	-	A03	-
	W-R	3	A10	A03	A02
<b>AK2/5</b>	N-M	3	A09	A01	A03
	M-E	0	-	-	-
<b>AK2/5/6/8</b>	D-V	1	-	-	A09
	V-K	3	A06	A02	A09
	K-L	3	A06	A02	A09
	L-Q	3	A06	A02	A09
	Q-X	3	A03	A02	A09
<b>Sum</b>	17	38	12	12	14

<sup>a</sup>chromosome.<sup>b</sup>genomic block association.<sup>c</sup>copy number of GB association in the *B. rapa* genome.**Supplemental Table 5.** Number of syntenic genes shared between each *B. rapa* subgenome and the *Arabidopsis thaliana* genome (At).

	LF	MF1	MF2
<b>#genes</b>	16,271	11,633	9,653
<b>#syntenic to At</b>	12,914	8,905	7,719
<b>#syntenic to At/#genes</b>	0.79	0.77	0.80

**Supplemental Table 6.** The frequency of tPCK-specific block associations in *B. rapa* and *B. oleracea*.

GB		<i>B. rapa</i>		<i>B. oleracea</i>	
Assoc.	#	Chromosome	#	Scaffold	
O-P	3	A02, A03, A09	3	Scaffold000203, Scaffold000059, Scaffold000335	
P-W	1	A03	1	Scaffold000168	
W-R	3	A02, A03, A10	3	Scaffold000032, Scaffold000030_P1, Scaffold000085	
D-V	1	A09		Scaffold000035_P2	
V-K	3	A02, A06, A09	3	Scaffold000254, Scaffold000170, Scaffold000135	
K-L	3	A02, A06, A09	3	Scaffold000006, Scaffold000126, Scaffold000048	
L-V	3	A02, A06, A09	3	Scaffold000006, Scaffold000045, Scaffold000049	
V-Q	3	A02, A06, A09	3	Scaffold000153, Scaffold000449, Scaffold000049	
Q-X	2	A02, A09	2	Scaffold000030_P2, Scaffold000150	

**Supplemental Table 7.** List of genomic blocks comprising the nine linkage groups of *Raphanus sativus* (Shirasawa et al., 2011).

LG1	LG2	LG3	LG4	LG5	LG6	LG7	LG8	LG9
S	S	F	N	E	E	A	O	C
N	F	B	I	W	W	B	J	A
E	H	A	J	P	R	U	W	C
N	F	M	I	O	P	S	R	B
E	D	N	S	M	O	C		A
R	X	C	V	R	Q	K		
	Q	H	L	X	L			
	L	X	Q	W	V			
	K	M	X	R	D			
	V	F	U	T				
	H			U				
	A							
	N							
	F							
	M							
	I							
	J							

**Supplemental References:**

Panjabi, P., Jagannath, A., Bisht, N.C., Padmaja, K.L., Sharma, S., Gupta, V., Pradhan, A.K., and Pental, D. (2008). Comparative mapping of *Brassica juncea* and *Arabidopsis thaliana* using Intron Polymorphism (IP) markers: homoeologous relationships, diversification and evolution of the A, B and C *Brassica* genomes. BMC Genomics **9**: 113.

Shirasawa, K., Oyama, M., Hirakawa, H., Sato, S., Tabata, S., Fujioka, T., Kimizuka-Takagi, C., Sasamoto, S., Watanabe, A., Kato, M., Kishida, Y., Kohara, M., Takahashi, C., Tsuruoka, H., Wada, T., Sakai, T., and Isobe, S. (2011). An EST-SSR linkage map of *Raphanus sativus* and comparative genomics of the Brassicaceae. DNA Res. **18**: 221-232.